

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Kriz, Alan L.

Luethy, Michael H.

Voyles, Dale A.

(ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXPRESSION OF
TRANSGENES IN PLANTS

(iii) NUMBER OF SEQUENCES: 28

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US Unknown

(B) FILING DATE:

(C) CLASSIFICATION: Unknown

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Highlander, Steven L.

- (B) REGISTRATION NUMBER: 37,642
- (C) REFERENCE/DOCKET NUMBER: DEKM:158

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (512)418-3000
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTGGAACTGG AACGGGCTTG GA

22

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCGAGGGCAA CGAGCAGCAC CTTCATGG

28

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTAATACGAC TCACTATAGG GC

22

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ACTATAGGGC ACGCGTGGT

19

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGCTCGAGGG ACCGGTTACA GCACACCACT G

31

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGTCTAGAGG TGTCGATCTT CTGTGCTCT

29

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCCATGGGG TGTCGATCTT CTGTGCTCT

29

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGACCGGTTA CAGCACACCA CTGTGGGTGG TCTCAAGGCA GTACCAAACCT ATAGCATCCA	60
TATAGCAGCA GAATCACCTG TCTTGTCTAC AAGACAGAAC CAATGCATCA ACTTCAAGGG	120
AGTACCAGCG TCTTCTTGAC TGTCTTTCAG AATTGTGGCA TTCTTGTGTTGG AAGCATAGCA	180
GTGTAGGTTG CTCATTCACG GATAATCTCG ACACGTAAAG TGATGAGGAA TACGGAACGA	240
CCATTGGCAT GTAGAGCTGT ATGAATTGGT GTTATCCATA CAACAACCTCG CAGAACATCA	300
CAAAATTGCA CGTCAATGGA TTGGGTCAGA AACAAATCGT CTCCTTGTAG CTTGTACAAT	360
GAAGTGATGG TGAGTCATGA GTCACACTGA TCCGATCTGA TATATATGCC AAATAGCTCA	420
CACGACAACA TTACAAACAA CCCCATACTA TACATCACAA AGTTTGTTC ATGAAAAAAC	480
AAATAAGTAT GCAGGAGGGG ACAATAATCC TTGCTTGACG CGTAAAGTGA ATTTACAAAG	540
CCATATATCA ACCTATATCT AATTAATAAG TTCGTTATAT ATACGCACGA TGATCATCAA	600
CAACCGTACC TGTGAAAGGC AACAAAATGA GCCACGCAAA AATGCAGAAT GAATCCATAT	660
GATGACGAAC GTACACTCGG CTTGCTACAT AAAGTGAATG ATGAGTCATA AATATTTGGC	720
AAGAAACCGT GAAAGCTACA CAGCCGTCGT CAGTAGCACA GGAACACAAG AACTGTGCT	780
AATCGAAGCT ATAAATAACC CTAGTATGCC TATGCACTTC TCCATCACCA CTACCCATAT	840
CTTCAGTCTA TTTACCTTCT CTATCTACTC CAGAGAGCAC AGAAGATCGA CACC	894

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTCAGCCCCA GCAGCCACAT CCA

23

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTGCGGCAGC CAATGACAAG TC

22

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACTGAAGAAA CTATATCCTA CTGTAATAAT AATGATGTAA TATAGCCGCT GGCGAGCTAA	60
GCTAGTTTAG TCATTTAGCG CGGCGATGGG TAATAAAAGT GTCATCCATC ACCATGGGTG	120
ACAATATATG CGAACAAATG ACCTGAAGAT GAACAATTGA AATGAAAAGG AAAATATATT	180
ACAATTCAAC GAGATATCCT CTCGATCGTA TCACGTGTCC ACAGGGGTGG ATCCATGCCC	240
CGGGCTGCCC GGGCTGCAGC CCGGGGCGTA GACCAAAAAT CCCTTTAGCG ATTCTTTTTT	300
TCAGTTCAAT TTTGCCAATA AAAACTACAT TTAGCCCTAC CTGATGCGGT CTAAAATTTT	360
TTTACACTAG TTTAGCCCCCT CCTGTAATGT GTTTCTAGAT CAGGCAATGT AT	412

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGCTCGAGGG ACCGGTTACA GCACACCACT G	31
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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TCAGTACTGG GCACCGCCGG C

21

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AAGGTGCTGC TCGTTGCCCT C

21

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGGAGCTCTC AGTACTGGGC ACCGCCGGC

29

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGAAGGTGC TGCTCGTTGC CCTCGCTCTC CTGGCTCTCA CTGCGAGCGC CACCTCCACG	60
CAAATAGGCG GCACGTGCGG CTGCCAACCA CCGCATCTGC CACCGCCGCC GGTTCATCTG	120
CCGCCTCCGG TTCACCTGCC CCCGCCGGTT CATCTGCCGC CGCCACAATG CCACTACCCT	180
ACTCAACCGC CCCGGCCTCA GCCCCAGCAG CCACATCCAT GCCCATACCA ACCGCAGCAT	240
CCAAGCCCGT TCCAGTTCCA GCAGCCGGGA ACCTGCGTTG GCCAAGGCAC CCAGATCCTG	300
GGCCAGTGCA TTGAGTTCCT GAGGCATCAG TGCAGCCCGG CGGCGACGCC CTACTGCTCG	360
CCACAATGCC AGGCGTTGCG GCAGCAGTGT TGCCACCAGC TCAGGCAGGT GGAGCCGCTG	420
CACCGGCAAC AGGCGATCTT CGGCGTGGTC CTGCAGTCCA TCCAGCAGCA GCCGATAGGC	480
CAGCCGCTCG CGGCGCTGAT GGCGGCGCAA ATAGCGCAGC AACTGACGGA GATGTGCGGT	540
GTGCGGCAGC CAATGACAAG TCCCTGCCCT TGCAGCGCTG CTGCCGGCGG TGCCCAGTAC	600
TGA	603

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGAAGAAGCA CGTACGCGGG CGGAACGCGT GTCCTGCCTG GATACGCGC GCGAGATGAC	60
GTGCGGCGGC GGC GCGCGAC TACCGCCGGC GCGGCATGGC CCTACTACGG CGGCTGCTGC	120
TGCTGCTACG TACGCTGCCG TAAAGTCTCG GTCGCCGTGC TAGCTCTAGC TAGTCGTTAT	180
GTGTGTTGTG CTTTGTATGT GCGCGTGTCT TGTTGGGACA TGCAGTGTAG TGCTGCTGTA	240
TGCGTG TGTC CTTTCTTGAT CGGAGTCGGA GTGGCTGATG CACAGCATGC TGGATGTCAA	300
GTTTATGATG AGGAATAAAA TGCAATGTTC AGGGCGAGAT ACTACGGTTT TCCTTGACTA	360
CCATGGGATT TG TAGAA	377

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCACTCGGCT TGCTACATAA AGTGAATGAT GAGTCATAAA TATTTGGCAA GAAACCGTGA	60
AAGCTACACA GCCGTCGTCA GTAGCACAGG AACACAAGAA ACTGTGCTAA TCGAAGCTAT	120
AAATAACCCT AGTATGCCTA TGCAC TTCTC CATCACC ACT ACCCATATCT TCAGTCTATT	180
TACCTTCTCT ATCTACTCCA GAGAGCACAG AAGATCGACA CC	222

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTAAGTATGC AGGAGGGGAC AATAATCCTT GCTTGACGCG TAAAGTGAAT TTACAAAGCC	60
ATATATCAAC CTATATCTAA TTAATAAGTT CGTTATATAT ACGCACGATG ATCATCAACA	120
ACCGTACCTG TGAAAGGCAA CAAAATGAGC CACGCAAAAA TGCAGAATGA ATCCATATGA	180
TGACGAACGT ACACTCGGCT TGCTACATAA AGTGAATGAT GAGTCATAAA TATTTGGCAA	240
GAAACCGTGA AAGCTACACA GCCGTCGTCA GTAGCACAGG AACACAAGAA ACTGTGCTAA	300
TCGAAGCTAT AAATAACCCT AGTATGCCTA TGCAC TTCTC CATCACC ACT ACCCATATCT	360
TCAGTCTATT TACCTTCTCT ATCTACTCCA GAGAGCACAG AAGATCGACA CC	412

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CATCGAGACA AGCACGGTCA ACTTC

25

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AAGTCCCTGG AGGCACAGGG CTTCAAGA

28

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2647 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TATGAATTAT TATGTATTTA TTAATTTTCA GTCGATTTAA AAAATAAAAAG AAAAGTAAAT	60
TGGAGATTTT ACATTGGGAA CCTAGAAAAT TTTTATTTT TTTTCTCTCT TCCATCGTAA	120
CGATTCTGGG CTGATTGGGC CTACAGAGAG GAGAGCGAAA GCGAAGTAAT ATGAGATTTT	180
ACATTAGGAA CCCTAGAATA TTTTTTATTT TGTTTTTCCC CTTCTAGAAA AGTTGGATGG	240
AGGAGGCCAT CGGTAAACCG AACACGGACA AGATCAGGGG CAAAAGAAAA TATTTGGCAA	300
ACTAAAATTT TGGCTCTTTA TAGATAGGTA TAGATTTGGG TTAAGAACAG TAGTCGGACA	360
TTCCACGCTT TGTTAAGTTC TTTTTTTACA TAACAAGAAT AGAATCACGC TCTGTAGGCT	420
CGTCAGACCG TACCTTTCTA AGGAAGTCGC TTTGGGTAGT TCAGTTGGCG AGAAAAGCCT	480
TCCTACCTTT GCAGGTCCAT CGGGCCGACT ACAACCCGTG GCTCAATCCC GGTTCCTGCG	540
GTGTCTTGGC AACATTCTTG TTGGAAGATA CCAGAAGGTT GCTCCACGGG TAATCTTGAC	600
ACGTATGTAA AGTGATGAGG AACATTGAAC GAACATTGGC ATGTAAGCTC TATAATTGGT	660
GTTATCCATA ACAACGTCGC AGAACATCAC AAATTGCACG TCAAGGGATT GGGTCAGAAA	720
CAAATCGTCT CCGTGTAACA CGAAGTGGTG AGTCATGAGC CATGTTGATC TGATATATAC	780
ATAGCACACA CGACATCACA AACAAGTCAT ACTACATTAC AGAGTTAGTT TCACCTTTCA	840
AGTAAAAACA AAGTAGGCCG GAGAGAGGAC AATAATCCTT GACGTGTAAA GTGAATTTAC	900
AAAGCCATAT ATCAATTTAT ATCTAATTCG TTTCATGTAG ATATCAACAA CCTGTAAAAG	960
GCAACAAATT GAGCCACGCA AAATTACAAG TGAGTCCAAA TAAACCCTCA CATGCTACAT	1020

AAAAGTGAAT GATGAGTCAT GTATATCTGG CAAGAAACTG TAGAAGCTAC AGTCATCGGT	1080
AGCAAAGAAA CACAAGAAAA TGTGCTAATA AAAGCTATAA ATAACCCTCG TACGCCTATG	1140
CACATCTCCA TCACCACCAC TGGTCTTCAT TCAGCCTATT AACTTATATC TATCTACTCC	1200
AGAGCAGACA AGAACTCGAC ACCATGAAGG TGTGCTCGT TGCCCTCGCT CTCCTGGCTC	1260
TCGCGAGCGC CGCCTCCACG CTTACAACCG GCGGCTGCGG CTGCCAGACA CCTCATCTAC	1320
CACCACCGCC GGTTCATCTG CCGCCGCCGG TGCATCTGCC ACCGCCGGTG CACCTGCCGC	1380
CGCCGGTTCA CGTGCCACCG CCGCCACCAC AATGCCACCC ACACCCTACT CTACCGCCCC	1440
ACCCACATCC ATGCGCTACA TACCCACCGC ATCCAAGCCC GTGCCACCCA GGGCATCCCCG	1500
GATCCTGCGG TGTGCGGGC GGCCCCGTCA CCCCGCCGAT CCTGGGCCAG TGCATCGAGT	1560
TCCTGAGGCA TCAGTGCAGC CCGGCGGCGA CGCCCTACTG CTCGCCACAG TGCCAGGCGT	1620
TGCGGCAGCA GTGCTGTCAG CAGCTCAGGC AGGTGGAGCC GCTGCACCGG TACCAGGCGA	1680
TCTTCGGCGT GGTCTGCAG TCCATCCAGC AGCAGCAGCC GCAAGGCCAG TCGTCACCGC	1740
TCCCGGCGCT GATGGCGGCG CAAATAGCAC AGCAACTGAC GGCATGTGC GGTCTAGGAG	1800
TGGGGCAGCC AAGTCCCTGC GCTTCTTGCA GCCCTTTTGC CGGTGGTGTC CACTATTAAA	1860
GAAACTATCT ATACTGTAAT AATGTTGTAT AGCCGCCGGA TAGCTAGCTA GTTAGTCATT	1920
CAGCGGCGAT GGGTAATAAT AAAGTGTCAT CCATCCATCA CCATGGGTGG CAACGTGAGC	1980
AATGACCTGA TTGAACAAAT TGAAATGAAA AGAAGAAATA TGTATATATGT CAACGAGATT	2040

TCCTCATAAT GCCACTGACA ACGTGTGTCC AAGAAATGTA TCAGTGATAC GTATATTCAC	2100
AATTTTTTTTA TGACTTATAC TCACAATTTG TTTTTTTTACT ACTTATACTC GAACAATTTG	2160
TTGTGGGTAC CATAACAATT TCGATCGAAT ATATATCAGA AAGTTGACGA AAGTAAGCTC	2220
ACTCAAAAAG TTAAATGGGC TCGGAAGCT GCGTCAGGCC CAAGTTTGG CTATTCTATC	2280
CGGTATCCAC GATTTTGATG GCTGAGGGAC ATATGTTCCG CTTAAGCTGC AGCTTTGTAG	2340
TTAGTTTTGT TTTTGATTAT ATTTAATACT CTATGCATGT GCACCAAGAT TTTTCTGGTG	2400
AATTAAACAA GGCCTAATAA CGTGAGTAGC GTATCTAACT GTGACCTATA AAGTAGAGCA	2460
CCTTTTTAGA GTAGGGGCTC CTTTTTTTAG AACTCTATTT ATTGCACCCA ACTTCAATAA	2520
GGGTCTTTTC ATCCAAAATT AAGAGTCCTT ACATTACATC TAATCGTCTA TTCATTGTCT	2580
ATATTTTAAT ATAAATCTTA CTGTATATCT TGTAGCACAC TAGTATGCCT CAAAGCCGAC	2640
AATAAAT	2647

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3704 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGGCGCCTG TACCGCGTGT GGGGACGATG AGCGCTCCCT GAACGCTGTC TTGGGAGAGC	60
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TGCAAGATGA GACACTCCAT CCCGCGCAGC CTGTCGTGGC GTCCTCCTGG ATGGACACCT	120
GCATCGCTGT CGCCCTCCAC CAACTCACCT GAACGAAGAA TAGAATAAAA AATGGAGGGA	180
GCTGAGGGGG CAGTGGTTGC GCTGTAGGGA GGAGAGAGAC CGCGTCATTA TAAGACTATC	240
TGCAACCGTT ACCTCTAAAT TTTTCCCTCT ATATCATTTT TTCCCCATAT TTTCCCCCT	300
ATTTTTTCAT CTCCCGCAAC GGTTCCTCCT AAATACTCCC CCTATATCTC ACTACCACTA	360
TAAAATATTA TTTTTTATAC CAACTATCAA TTTTTTATCT ACTAACAATT ACTCGTGGAC	420
CCACAGCACA GTGTTTAGGA GATGAACAGT GACACGCTAT ATCTGGGGGG AGAGAGAAAG	480
AGGCGCGCGT AGGGGGCGCG CGGTAGGGGC ACTGCTGCGG CTGTAGAGTA CCCCCTACAC	540
GCCGGCATGC AAGGGAAGGG GGCAATGTTG CGCATAGCCT AAAGAGCGGA TGAAGCGGCT	600
TGCAATTTGC ACGCTGGATT CATAAATAGT GCATATTACT AAAAAAAGGG TGGGGACGTA	660
GGTATAGAGA GTCTATTAGA GTTGATCTAA GACCCGGTTT ATTTAGATT ATAATCTGTC	720
CGGATTATAT AATCCAGCGC AAATAATACA GTAGGTAAAC AAACAAC TAG ATTATGGGTT	780
CAGATTATAT AATCTAAACC CCAGATTATG ATAATCTCAT AATCTCCTCA AGAGTAGCTT	840
ATTGGAGATT ATTTTGGCAA AAGACCCACT ACCCATGGTT ATGTAAATAG AAATTATAAT	900
ATATATCATC TTTTTTCTCA CCTTAAATAA ACAAATAAGG GTATTGTTGT CTTTATGAAT	960
AATCTACATT TGTATAATCT AACTACCAA ACAACTACAT CTAGATTATA ATCTGGATTA	1020
TATAATTTAA ATTATAATCT AGATTATATA ATTTATAAGC TGAAACAACC CGGCCCTAAA	1080
GCACTATCGT ATCACCTATC TGATAGTCAC GGGTTTCGAA CGTCCACTTG CGTCGCACGG	1140

AATTGCATGT TTCTTGTTGG AAGCATATTC ACGCAATCTC CACACATAAA GGTTTATGTA	1200
TAAACTTACA TTTAGCTCAG TTTAATTACA GTCTTATTTG GATGCATATG TATGGTTCTC	1260
AATCCATATA AGTTAGAGTA AAAAATAAGT TTAAATTTTA TCTTAATTCA CTCCAACATA	1320
TACGGATTGA GTACAATACT CATGTGCATC CAAACAACT ACTTATATTG AGGTGAATTT	1380
GGATAGAAAT TAAACTAACT TACACACTAA GCCAATCTTT ACTATATTAA AGCACCAGTT	1440
TCAACGATCG TCCCGCGTCA ATATTATTAA AAAACTCCTA CATTTCTTTA TAATCAACCC	1500
GCACTCTTAT AATCTCTTCT CTACTACTAT AATAAGAGAG TTTATGTACA AAATAAGGTG	1560
AAATTATGTA TAAGTGTTCT GGATATTGGT TGTTAACCTC ATATTACAC AACCTAATCA	1620
ATAGAAAACA TATGTTTTAT TAAAACAAAA TTTATCATAT ATCATATATA TATATATACA	1680
TATATATATA TATATATATA TAAACCGTAG CAATGCACGG GCATATAACT AGTGCAACTT	1740
AATACATGTG TGTATTAAGA TGAATAAGAG GGTATCCAAA TAAAAAACTT GTTCGCTTAC	1800
GTCTGGATCA AATTGGGTTG GAAACGATTA AATCTCTTCC TAGTCAAAAT TGAATAGAAG	1860
GAGATTTAAT CTCTCCCAAT CCCCTTCGAT CATCCAGGTG CAACCGTATA AGTCCTAAAG	1920
TGGTGAGGAA CACGAAACAA CCATGCATTG GCATGTAAAG CTCCAAGAAT TTGTTGTATC	1980
CTTAACAACT CACAGAACAT CAACCAAAAT TGCACGTCAA GGGTATTGGG TAAGAAACAA	2040
TCAAACAAAT CCTCTCTGTG TGCAAAGAAA CACGGTGAGT CATGCCGAGA TCATACTCAT	2100
CTGATATACA TGCTTACAGC TCACAAGACA TTACAAACAA CTCATATTGC ATTACAAAGA	2160

TCGTTTCATG AAAAATAAAA TAGGCCGGAC AGGACAAAAA TCCTTGACGA GTAAAGTAAA	2220
TTTACAACAA AAAAAAGCC ATATGTCAAG CTAAATCTAA TTCGTTTTAC GTAGATCAAC	2280
AACCTGTAGA AGGCAACAAA ACTGAGCCAC GCAGAAGTAC AGAATGATTC CAGATGAACC	2340
ATCGACGTGC TACGTAAAGA GAGTGACGAG TCATATACAT TTGGCAAGAA ACCATGAAGC	2400
TGCCTACAGC CGTCTCGGTG GCATAGGAAC ACAAGAAATT GTGTTAATTA ATCAAAGCTA	2460
TAAATAACGC TCGCATGCCT GTGCACTTCT CCATCACCAC CACTGGGTCT TCAGACCATT	2520
AGCTTTATCT ACTCCAGAGC GCAGAAGAAC CCGATCGACA CCATGAGGGT GTTGCTCGTT	2580
GCCCTCGCTC TCCTGGCTCT CGCTGCGAGC GCCACCTCCA CGCATAACAG CGGCGGCTGC	2640
GGCTGCCAGC CACCGCCGCC GGTTTCATCTA CCGCCGCCGG TGATCTGCC ACCTCCGGTT	2700
CACCTGCCAC CTCCGGTGCA TCTCCCACCG CCGGTCCACC TGCCGCCGCC GGTCCACCTG	2760
CCACCGCCGG TCCATGTGCC GCCGCCGGTT CATCTGCCGC CGCCACCATG CCACTACCCT	2820
ACTCAACCGC CCCGGCCTCA GCCTCATCCC CAGCCACACC CATGCCCCGTG CCAACAGCCG	2880
CATCCAAGCC CGTGCCAGCT GCAGGGAACC TGCGGCGTTG GCAGCACCCC GATCCTGGGC	2940
CAGTGCGTCG AGTTCCTGAG GCATCAGTGC AGCCCGACGG CGACGCCCTA CTGCTCGCCT	3000
CAGTGCCAGT CGTTGCGGCA GCAGTGTTGC CAGCAGCTCA GGCAGGTGGA GCCACAGCAC	3060
CGGTACCAGG CGATCTTCGG CTTGGTCCTC CAGTCCATCC TGCAGCAGCA GCCGCAAAGT	3120
GGCCAGGTCG CGGGGCTGTT GGCGGCGCAG ATAGCGCAGC AACTGACGGC GATGTGCGGT	3180
CTGCAGCAGC CGACTCCATG CCCCTACGCT GCTGCCGGCG GTGTCCCCCA CTGAAGAAAC	3240

TATGTGCTGT AGTATAGCCG CTGCCCCTG GCTAGCTAGC TAGTTGAGTC ATTTAGCGGC	3300
GATGATTGAG TAATAATGTG TCACGCATCA CCATGGGTGG CAGTGTCAGT GTGAGCAATG	3360
ACCTGAATGA ACAATTGAAA TGAAAAGAAA ATACTCCATC TGTTCCAAAT TAAAATTCAT	3420
TTTAACCTTT TAATAGGTTT ATACAATAAT TGATATATGT TTTCTGTATA TGTCTAATTT	3480
GTTATCATCC ATTTAGATAT AGACAAAAAA AAATCTAAGA ACTAAAACAA ATGCTAATTT	3540
GAAATGAAGG GAGTATATAT TGGGATAATG TCGATGAGAT CCCTCGTAAT ATCACCGACA	3600
TCACACGTGT CCAGTTAATG TATCAGTGAT ACGTGTATTC ACATTTGTTG CGCGTAGGCG	3660
TACCCAACAA TTTTGATCGA CTATCAGAAA GTCAACGGAA GCGA	3704

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGCTCGAGTA AGTATGCAGG A	21
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(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGCTCGAGCA CTCGGCTTGC T

21

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CGGGCTGATC CTGGCCGGCA CCGT

24

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GTGTTCTCCT GGATGTACAA GTAC

24

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TCCAAGGCC GCGACGTCAA GGAAC

25